

ABSTRACT OF THE DISCLOSURE

Using contextual response profiles to group genes into “equivalent” classes to infer biological functionality. Comparing such classes from different contexts (conditions) to identify genes that change functionality. Also, methods, systems and computer readable media to separate gene expression signatures and distinguish differential gene expression specific to pure tissue in a heterogeneous tissue sample. Further, methods, systems and computer readable media for validating or calibrating a plotted curve of sorted p-values is provided. Still further, methods, systems and computer readable media are provided for distinguishing differentially expressed genes based on plotting expression levels and replicates derived from one or more genes in a first sample against corresponding expression levels and replicated derived from one or more genes in a second sample.